

Figures for main text

Are ecological communities the seat of endosymbiont horizontal transfer and diversification? A case study with soil arthropod community.

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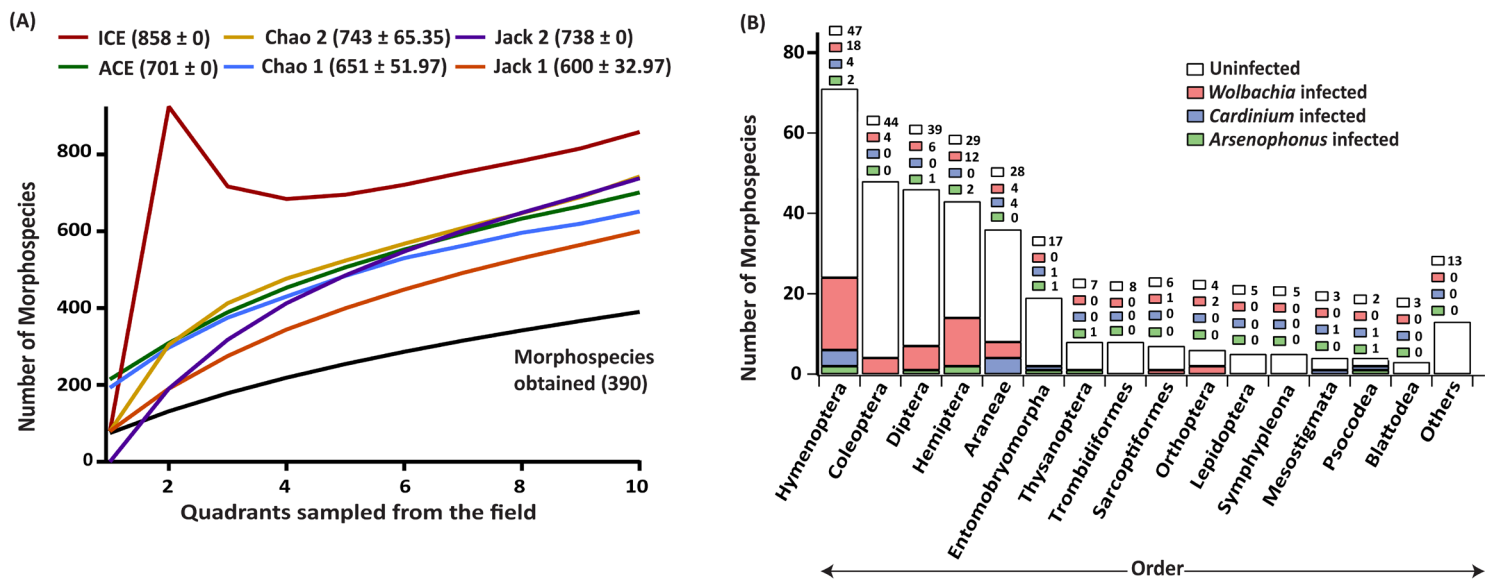


Figure 1: A) Rarefaction curve of morphospecies found (in black) showing species richness in the soil arthropod community. Colored lines represent expected number of morphospecies. B) The distribution of three endosymbionts screened across different host arthropod orders.

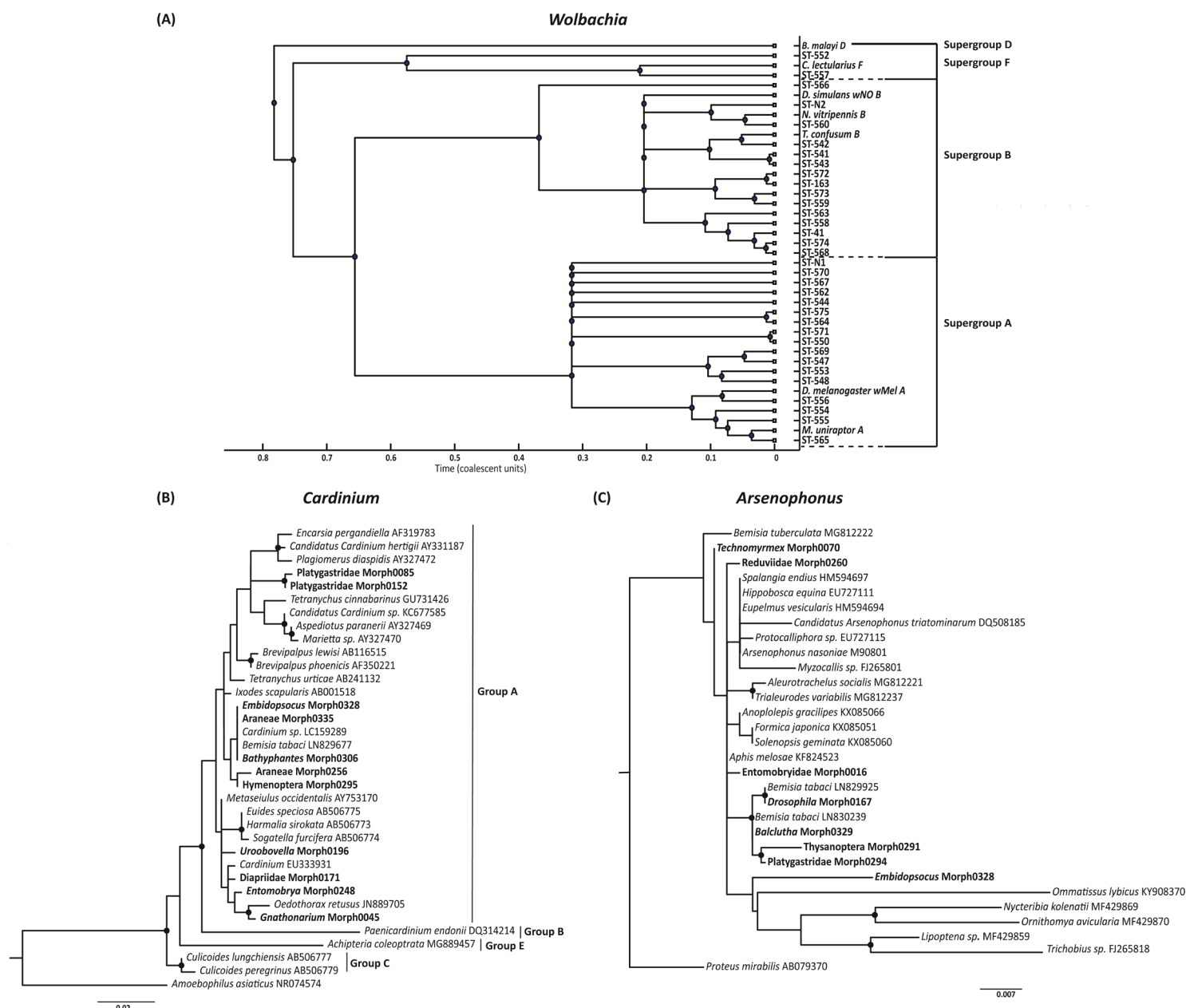


Figure 2: Phylogenetic analysis of (A) *Wolbachia*, (B) *Cardinium* and (C) *Arsenophonus* found, shown with some known sequences for better resolution. *Wolbachia* phylogenetic tree was constructed using MLST data in ClonalFrame with 50% majority rule consensus. *Cardinium* and *Arsenophonus* phylogeny was made in MEGA7 using 16S *rRNA* gene fragment. Dotted nodes represent bootstrap value >50. *Wolbachia* infections are shown as STs whereas *Cardinium* and *Arsenophonus* are labelled with host taxa that they infected. Infections obtained in this study are in BOLD. *Brugia malayi*, *Amoebophilus asiaticus* and *Proteus mirabilis* were taken as outgroup for *Wolbachia*, *Cardinium* and *Arsenophonus* phylogenetic analysis, respectively.

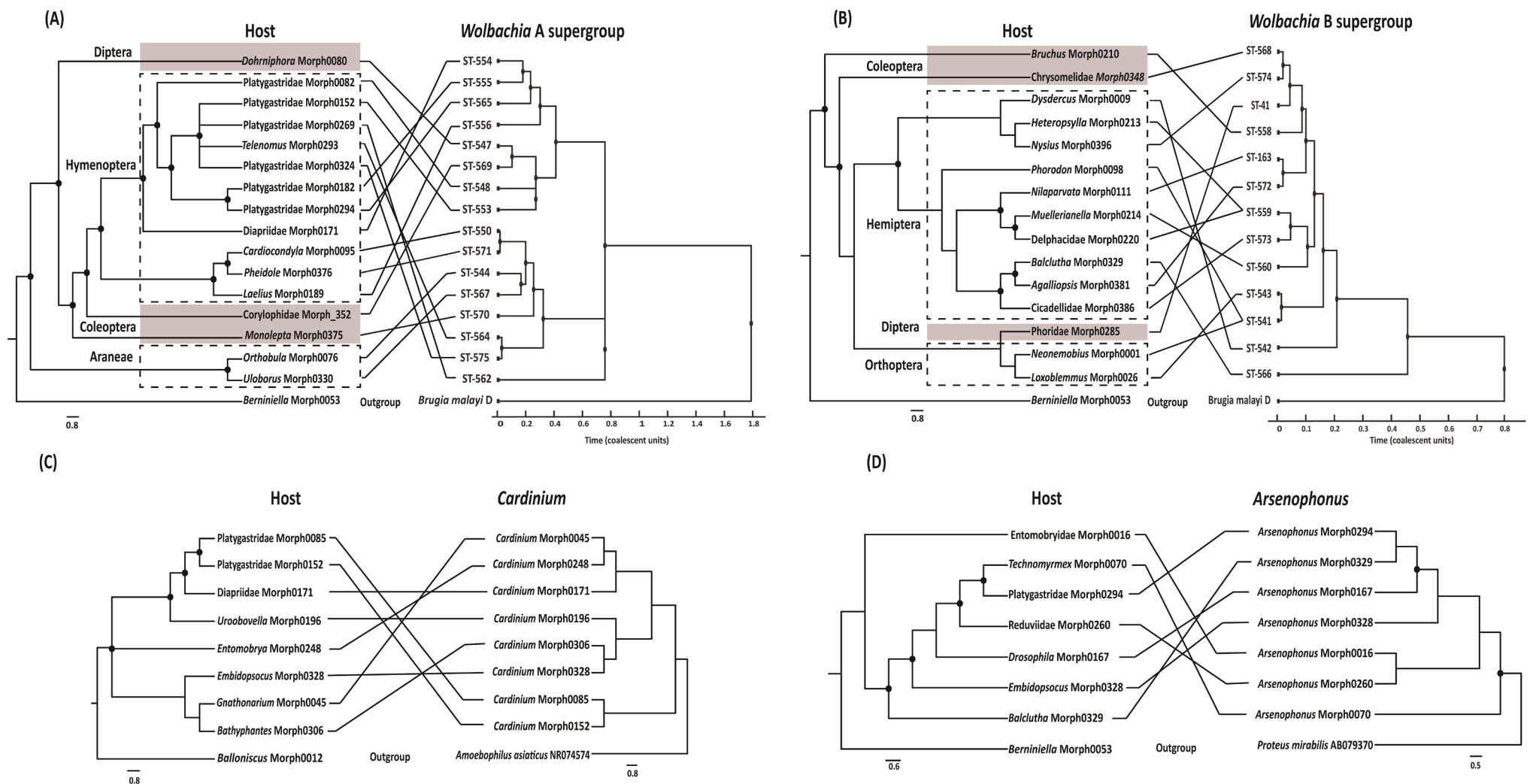


Figure 3: Association between infected host (left) and endosymbiont (right) phylogeny with (A) *Wolbachia* A supergroup, (B) *Wolbachia* B supergroup, (C) *Cardinium* and (D) *Arsenophonus*. Host phylogeny was constructed by MrBayes using partial *CO1* sequences. Black dots represent clade credibility value >70. Phylogenetic relationship between different *Wolbachia* strains was interpreted through ClonalFrame. *Cardinium* and *Arsenophonus* 16S *rDNA* phylogeny was constructed using MEGA7. Correlation between the two phylogenies suggest phylogenetic incongruence and extensive horizontal transfer across host taxa.

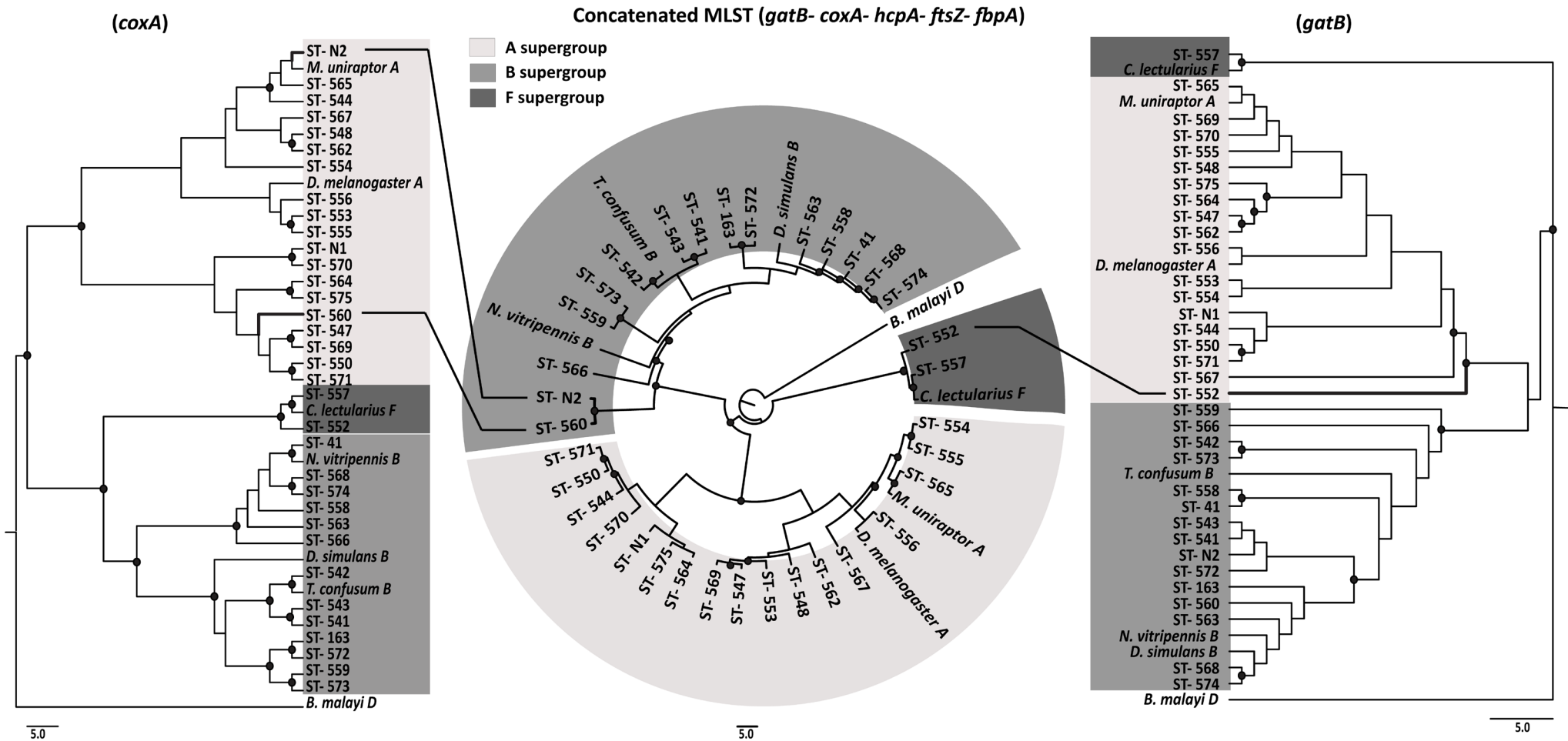


Figure 4: Maximum likelihood phylogenetic trees of *coxA* (left), concatenated MLST dataset (centre) and *gatB* (right) gene made using MEGA7. Black dots represent bootstrap value >50. *Wolbachia* ST-N2 and ST-560 clustered with B supergroup in concatenated MLST phylogenetic tree whereas in *coxA* phylogenetic tree, these strains clustered with A supergroup indicating recombination between *Wolbachia* supergroup A and B. Similarly, ST-552 clustered with F supergroup in concatenated MLST tree, but the individual *gatB* gene tree shows it to be from A supergroup, indicating recombination between A and F supergroup. These three cases (ST-N2, ST-560, and ST-552) represents between supergroup recombination of gene or gene segment.